

**Supplementary Figure 4.** Heat map based on RNA-seq of selected differentially expressed genes detected in microarrays. Triplicate cultures were harvested at day 1 and 7 and RNA was extracted and process for RNA-seq as described in materials and methods to validate the microarrays. P value adjusted for multiple testing using Benjamin-Hochberg procedure (P<sub>adj</sub> is shown in Supplementary Data set 4.